

SEQUENCES OF SELECTED REGIONS OF APTAMERS AGAINST D-AMINO ACID AB1-40 TARGETS 1,2,3

5 Target 1 (MONOMERIC)

SEQ ID NO:1

GGA CGA AGA GCG TTA TCT TAC GCT GAC TGG ATA TTA GTT TGT TGG AAT AC

10

SEQ ID NO:2

TCG TTA TTC TGT TCA GGG TTT GAG ACT CGT TGT ATC GAT TTA G.. ..

15

SEQ ID NO:3

GGC CCC TAT ACG AAC GTC ATC GTA CTC AGC TGT TGT TGT CC. ....

SEQ ID NO:4

20

TTT ATA TCG CTT CCA CGT GTT TTA CCC ACA CCT TGT TTT AGC GGT AA.. ..

SEQ ID NO:5

25

TTA ATG ACG CTG TAC ATG GGA TCG TAT AGT GCC ACA GGT AAA TCT GCA TG

SEQ ID NO:6

CTG TTC TTA TCA AGC CAA ATA AAG TAC TAT GCC CTA AGG CCT ATA TGA TC

30

SEQ ID NO:7

CGG TGG GAA ATA TCT TTG GCT GGC TTA GTA ACT TCG TAT TTG CTC GGC TG

35

SEQ ID NO:8

TTG TCC ATT GTA TAC GAT GCG CTT CAA GGA TGA TAC GGC TTT CAC GCA ..

SEQ ID NO:9

40

TCC CTT AGC AGG CTT CAT TTC CTT GAC CAT TCT TTG CGT TGA GCC TGT CT

SEQ ID NO:10

5 AAA CGA GTA TCT TTT TGG GAT CTT TCA GCT GCT AGT GCA ATA TCA TCT CT

SEQ ID NO:12

0 TGG TCC TGC GAC CAG CAG TCA ATT AGG GTT TAG CAC AGT AGA GGC CT.

SEQ ID NO:13

5 CGC GAC TAA CTT GCG TCA GTT TTG TAC GGG TGT TTA GCT CCC TTT TA.

SEQ ID NO:14

5 TTC TCT CAC TTC CTT CCA GGT GAA CGG CGC ATT AAG GTC TTG TTG AT...

SEQ ID NO:15

10 CAG AGT TAG ATG GCA GCT ATT GTC GCC TAAGTT TGC TTT ATA TCA TCT TT

SEQ ID NO:16

15 CGG CGC GTC CCT GCA AGT CAA CTG TTT CCT GGC TCG CTT TAC GAT  
CCT TT

Target 2 (PRE-FIBRILLAR)

5 SEQ ID NO:17  
CGT ACA CAT CAA ACT TTC GAA TCC ACA GGA TAA TCG AGG AGA TCT CCT GA

10 SEQ ID NO:18  
TTG TCG CGA TAC TAC ATT TGT CCT GTC TGT GTG TCA TAC GGA ACT  
GTG TA

15 SEQ ID NO:19  
CGC CCG TCG ATT TGA AAC ACT CTT CAT CGG CGT TAA CCA CGG CGT GGA GA

20 SEQ ID NO:20  
CGT ACC GCG CTA CGT TCC CAT AAG CGT GCA ATT TGT TTG CCT TGG GTT GG

25 SEQ ID NO:21  
CTT TCA AGG TGG GGA TAC CGA GAC AAT TAG TCA TCT GTA GTGT GAT CAG T.

30 SEQ ID NO:22  
TAG AAG CGT CGA ATC ATT GGG AAT TCG TGC ATT TAG GGC AGG CAC TTT GG

35 SEQ ID NO:23  
CAA GCG AAA TGT CAC TGT GTA AGG TGT AAC AGG GAA CAA GGG AGG ACA A.

40 SEQ ID NO:24  
GGT ACT TGT TTT CGG TAC TTT GGT GCT TTG GGA CCA CGG TTT GAT GGT GT

45 SEQ ID NO:25  
TGC GCG GAG TTT CTA TTT GTG TAT GGC GTT CCT TAT CTA GGG CAG ACT IC

50 SEQ ID NO:26  
TTT GTA CAG TGC TTT CGC TTG TCT TCG CAG CGC GCT AAT TGC TTG CGA GT  
SEQ ID NO:27  
GAG CTC AGT GGG GTC TTG GTA GGT TAG AAG AAG TAG CTA TGG CTT TCG AA

55 SEQ ID NO:28  
CGT GAT AGC CCA CGG TCA AGG GTC TAC GAG TCA TTT GTT CCT AAC GCT GC

SEQ ID NO:29  
CAA GGA GGA TAT ATG CTT GGG ATC AGT CGT GTT GTT GAT ATT TAT GAT GG

SEQ ID NO:30  
AGG CTG CAG GCT TGG ATG GTG CTT CGG GGC GTC GTC TTA TTG CCT GCT AC

SEQ ID NO:31

5 GCC TCG GTG TGT TAA GGA GGA AGA GCG CCC ATC TCA GCA GTT ACC GGT CG

SEQ ID NO:32

CGC CCC GTC GAT TTG AAA CAC TCT TCA TCG GCG TTA ACC ACG GCG TGG AG

10

SEQ ID NO:33

CGG ACT GAG CAT TAG TTC GTG TCA CAG CGA CGT CGT TGT GTA AGG CTG AA

15

SEQ ID NO:34

TCC TGC CAA GCT CCT TTT TTT GGT AGT GAA TTT CCT TTA TCC TGG GGC GA

20

SEQ ID NO:35

CTA AAG TAT GTG TTA GTA TGG CCC TGC TTA TTA ATG TCG GGA GTT CGG ..

25

SEQ ID NO:36

TAG AAG CGT CGA ATC ATT GGG AAT TCG TGC ATT TAG GGC AGG CAC TTT GG

Target 3 (PROTOFIBRILS)

SEQ ID NO:37

TAA AGT GCG GAC TCA GGG AAT AAG GTG AGA ACT GAC CAA GGT GTG TGT TG

5

SEQ ID NO:38

TCG ACT TTT GAC AAG CAT CTC TTT TAC TGA GAG TTG GGA GGG AAC GGA TG

10

SEQ ID NO:39

GGG GTG CTA AGC ATT TGG CAT CCG TTT TGT GAA CTG CTC GAT GTT TAT TC

15

SEQ ID NO:40

TTA ACT GCA CCT TGC AGT AAC TAC AGG ATA GCA GTC CTA GAG CCA GTC AT

20

SEQ ID NO:41

TGC ATT ACC AGG GGA TAA CCT CGC ATT TGG CGG GTT AGG AGT AAC GTG CA

SEQ ID NO:42

ACT CTC GGT ATA TTG TTA GAT TGG GAG CGA CGC GTC ACC GTA TGA CAT GT

25

SEQ ID NO:43

GGT TAG CGG GGT TAC CTA ACA TCA GCT CTA GTT AGA CCT TTT TTT ACA AC

30

SEQ ID NO:44

CGA ATG CTT CGT AGT AAG TAA TGA ATC TTT TTG ACA CAC TAA TCG TAG GA

35

SEQ ID NO:44

GTC CCG TCC ATA GTG CTC GCC ACC ATT TCC TTT GGG TCA GGA ATT AGT TC

SEQ ID NO:45

TGG GAG AAG GAC TAG CTC GTT ATT GGT CAT GTT AGT CAT AGC CTG ACA CC

40

SEQ ID NO:46

CGG GGC ATA GTA CAG AAT CTT AGT GGG TGT TCT TTG ATT CTG GAG GAG CA

45

SEQ ID NO:47

GTG TGT TTT TAT CTA CTG GTC GGT GGT TTG GTT GGT AAT GCT TAA GCG GC

50

SEQ ID NO:48

TTG GAA CCC AGT GTG TTT TAC ACG CTC ATC TTT GCA ACA GGG TGT GTG AC

55

SEQ ID NO:49

ACG GTT AAC AAT CAT GGG CAA GCT CTT AGA ACA GCG TTC TGC GAT TTA CGA

SEQ ID NO:50

5 GAC GCC GCC GGG GAG CTC TAA ACG GAT TAC CAT TTG TCG GTG GTC TTA TT

SEQ ID NO:51

10 GCA TAG GAT TTC GGT TGG GAT AGA TAT TAT TCG GTT TCG ATC ATA CGT AT

SEQ ID NO:52

15 CTC ATA GGG ATG GTC TCC CGC TGG GCT TTT TCT GTT AAC AIT TAG AAC TC

SEQ ID NO:53

20 CAG GCC GCC GGG GAG CTC TAA ACG GAT TAC CAT TTG TCG GTG GTC TTA TT

SEQ ID NO:54

25 TCA CGT GTG CTG TAC GAC TGA TGT TTT TGC TGC CAG AATG ACT AGA AAT  
GT

SEQ ID NO:55

30 ATC GTA AGT GAT TGT TGT TTT ACA TGG CCT CCA GTT GGG GAG TCT TCC AC

30

SEQUENCES OF CONSTANT FLANKING REGIONS (AT 5' AND 3' ENDS) OF  
INSERTS

5' end of top strand (primer 1) SEQ ID NO:56

35 5' AAT TAA CCC TCA CTA AAG GGA ACT GTT GTG AGT CTC ATG TCG AA.....

5' to 3' end of top strand (complementary of primer 2) SEQ ID NO:57

40 .....TTG AGC GTC TAG TCT TGT CTC CCT ATA GTG AGT CGT ATT

SEQUENCES OF SELECTED REGIONS OF APTAMERS AGAINST  $\beta 2m$ .

Primer 1 SEQ ID NO:58

AGTAATACGACTCACTATAGGGCCAAGCTTGCATGCCTGCAG

5

Primer 2 SEQ ID NO:59

GGTACCGAGCTCAGGTTCCC

SEQ ID NO:60

10 NATTAGCGAACATAGTAGNGAAAGAAAGNACAGCANGAGGGGCT

SEQ ID NO:61

15 GTTGGTTACGCGTACAGTGAAACTCGGAAAGTTGAAGGGCCAAATGGGAAC

SEQ ID NO:62

GAGCAGCACCGGGCCACGGCGCAATCACCTAAAATCGGAGCCGCCGGGTGCAGCATGTG  
AC

20

SEQ ID NO:63

GGCNTGACANGGCAGGATAGCCGGNCNANGCGANCNNTNGGNCCNCGANACCCGACNGT  
GG

25

SEQ ID NO:64

GGTACCGAAAAGTCATTGGTTACAACCAGGCAGGCGCAGGAA

30

SEQ ID NO:65

GAATGGGCGAGTTGAGCGACTGAGGCAGCATGGAATCATACGTAC

35

SEQ ID NO:66

GGAGGCCGAGAGGGCAGAACCCAGCGACGCGACGGAAAGACCATAACGGCAGC

SEQ ID NO:67

40 GCACACGGGCGCACCCCTGCGAAACGACTATACGTCACTAGAGCAGGTTTGCGGAGTCC  
C

SEQ ID NO:68

45 GTGCGAGCAGGGCAACCAGAAGAAAACGTAGGTAGAGTGTCGAGTTGATGAGACGT

SEQ ID NO:69

GCCGCAAGAACGGGAGAAGAGCGGAGAACGTTGAACCGACCGGAGG

50

SEQ ID NO:70

GTAGAGTGTTGGGCTAGCGTGACCAGACATCTACGTGGGCAGGGAGCATTG

SEQ ID NO:71

55 GGAGGGGCCGTAAACGCGAACGAGACAACCAGATAAGGACCGCCCAATGAGAGGAACGGC  
AA

pH3.6 induced  $\beta$ 2m fibrils (Immature Fibrils)

- 5 SEQ ID NO:72  
AGTAATACGACTCACTATAGGGCCAAGCTTGCATGCCTGCAGATGAGAATACACAGAACA  
GAGGAGAAGGGGATGAATCAATAAGGTCACACTAACCAACNCGGTACCGAGCTCAGGTT  
CCC
- 10 SEQ ID NO:73  
ATGAGAATACACAGAACAGAGGAGAAGGGGATGAATCAATAAGGTCACACTAACCAACN  
C
- 15 SEQ ID NO:74  
AAAAATAAANTGTGTACACNAAANNGCNANCCCCNGGAANGAANGNCAACAAANGTNA  
GT
- 20 SEQ ID NO:75  
GGGAGAATTATGGAGTTTGTAAAACATTGGTCAGTGGCAGAGGTTTCATCACCGTCATC
- 25 SEQ ID NO:76  
ACACCTGGAATTAAATTCAGGACACCCAACGCGCCTACGAATAGAGCGGGAACGACGAC  
C
- 30 SEQ ID NO:77  
CGGAAGAGCACAAAAAAGGGGACTCGCCTTGGAAGGAACNTGC
- 35 SEQ ID NO:78  
TTACGTCNGGCCTNAACGAATGAACGGGGAAAGNAAGGAATGATTGGGANCATANACAG  
N
- 40 SEQ ID NO:79  
GGAGTGTGGATATGA
- 45 SEQ ID NO:80  
ACACGGAGGCACCTACAGTACTGGGGCAGGAGTTGCGCAGAGGACTAGTGAAAAAGGAG  
T
- 50 SEQ ID NO:81  
GCCAGCACGACAAANAGCAGGACGTAAAGAAGACGAAAGGGAGAACATTCGGGGAGAC  
GA
- 55 SEQ ID NO:82  
CCTGGGATCTCCAGGGGGCGGCGGAGCGATAGGTGTGCGTGAGTTGAAAAGGCAGGGCA  
A



SEQ ID NO:83

GAGACAAGTCGGTAGGACAGAGGAGTGAACAAAAGAAGCAGAGAGGAGAGTCAGAGCA  
GC

5

SEQ ID NO:84

ATCTACCGGTTACAAATCAAGAGAACTATTTTGTATGAGCCACTTATCTCTCCTGAAGT

10

SEQ ID NO:85

CGCANGAAATATAAACGTGGGGAGGACCAGGGGAGAGTACTCCAAAGAGTGAAGAAGGT  
T

15

SEQ ID NO:86

GCGGTAGAATGCATGGCGATTGCGATTGTAGGATTCCGCATCACACCTCC

20

SEQ ID NO:87

AAAAGGACAGGAGC

SEQ ID NO:88

ACTATAAGTNAGNNGGAGGGGGANCATGAAACAATNGTTTAAGAACGTANANTGGNTGA

25

SEQ ID NO:89

ACACGGAGGCACCTACAGTACTGGGGCAGGAGTTGCGCAGAGGACTAGTGAAAAAGGAG  
T

30

SEQ ID NO:90

AACGAAATGATAACAACAAATACACACGTCACACCGAAGTTGACCCAAGACTC

Aptamers against  $\beta$ 2m mature Fibrils

SEQ ID NO:91

5 ATTAACGAGANTGAAGGAAANCGGGAGGGAGANCAGGCACAACGGCGACANGAAAAGA  
GAGAGTGCGGTANCCG

SEQ ID NO:92

10 CCGAGGCCGCACACATAAGGGGGAGGGAAAGACAGCAGAATAAANAGGAGGCGATAGT  
NC

SEQ ID NO:93

15 GGTAAGGTGGAAGGGAAAAGGAAACGGAATGAACCCGCGTTATGGCCGAAAAGGGAC

SEQ ID NO:94

20 GAACAGGACGCGTAGCCCTACGATCCA

SEQ ID NO:95

CGAGGACGAAANAGTTTAGAAAAGGAGACGGCGCTTCGAACGAACCATCCCCTAGGT

SEQ ID NO:96

25 AAGTGANNAGGCAAAAGGAAAAAAGGTGAACAAGGCTGCTC

SEQ ID NO:97

30 GGCCCCACGAAGTGGGGGGAGGAACGTTNGTGTTGAGTGATTGGAGTNCCCTGGGCGA  
AATCC

SEQ ID NO:98

35 GCAAACGGGGGCGTTTCGGCGGAGGAGTGGAAGAAAAACGAGAGAAGAGTTGGAACG

SEQ ID NO:99

40 GCANGGGGAANGGGATTGAACGAGAAGAAGGAGGAGC

SEQ ID NO:100

45 GCACCTTICTCACTTTNNGGGCACAAAACCGCGCACCGGGCTAGNCTGGAGTGGGATGAA  
CGAC

SEQ ID NO:101

50 TGAGGGGAGGTTGGCGGAAGGCGAGGCAGCACGACCAGAAGTTTTTGAGTTCGAGAGG  
GGAT

SEQ ID NO:102

55 CCTGGAGGAGGGCAGCGNCGAGAAGGGGAAAAAAGAAAAGAACTATTCGTGGAGCGG  
AT

SEQ ID NO:103

GAAAAGGAGGGGATTNAAATCGCGTGAAAGGTGAATTGTTGCCAGGGGCGAATNCGG  
T

5

SEQ ID NO:104

GGGGCTTCATNGAGAGAAGGAACACAGACGAAAAAAGGGGGGNGTTCAAGAGGAA  
GAGACCGA

10

SEQ ID NO:105

GTGTAAGCTTGCGTCGAAGATGAANAAAATGTCGAATCCTCGCTGTGCCGCCAGACGTGA

15

Downstream primer (SEQ ID NO:106)

[5' TAA TAC GAC TCA CTA TAG GGA GAC AAG ACT AGA CGC TCA A...3'] (SEQ ID  
NO:106)

20

Random 50 mer (SEQ ID NO:107).

[5' AAT TAA CCC TCA CTA AAG GGA ACT GTT GTG AGT CTC ATG TCG AA-N<sub>50</sub> TT GAG  
CGT CTA GTC TTG TCT 3'].

25

JAN01P1 (SEQ ID NO:108)

5'AGT ATT ACG ACT CAC TAT AGG GCC AAG CTT GCA TGC CTG C3'

JAN01P2 (SEQ ID NO:109)

30 5'GGG AAC CTG AGC TCG GTA CC3'

JAN01T (SEQ ID NO :110)

5'CCA AGC TTG CAT GCC TGC AG N<sub>60</sub> GGT ACC GAG CTC GAA TTC CC3'

35

SEQ ID NO: 111

FYLLYYTE

SEQ ID NO:112

DWSFYLLYYTEFT

40

SEQ ID NO:113

DWSFYLLYYTEFTPTKDEYA